



SEQUENCE LISTING

<110> Munroe, Donald
Gupta, Ashwani
Vyas, Tejal
Chun, Jerold

<120> MAMMALIAN EDG-5 RECEPTOR HOMOLOGS

<130> 2931-105 (new); P108074-00003 (old)

<140> US 09/581252
<141> 2000-12-04

<150> PCT/CA 98/01193
<151> 1998-12-24

<150> US 08/997803
<151> 1997-12-24

<160> 29

<170> PatentIn version 3.2

<210> 1
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Degenerate PCR primer: A1

a1
<220>
<221> misc_feature
<222> (1)..(32)
<223> n = i

<400> 1
aaytrsatnm tnstnaayyt ngcngtngcn ga

<210> 2
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Degenerate PCR primer: B1

<220>
<221> misc_feature
<222> (1)..(33)
<223> n = i

RECEIVED

JAN 24 2003

TECH CENTER 1600/2900

32

<400> 2
ctgnykwttc atnawnmmrt anaynayngg rtt

33

<210> 3
<211> 639
<212> DNA
<213> Artificial Sequence

<220>
<223> Murine edg-5 RT-PCR clone 501

<220>
<221> misc_feature
<222> (126)..(628)
<223> n = unknown

<400> 3
aacactggcc cgggtgtcgaa aacgttgacc gtcaaccgct ggttcctccg ccaggggctc 60
ctagacacca gcctgactgc ctccctggcc aatttgctgg ttattgctgt ggaaagacac 120
atgtcnatca tgaggatgag agtccacagc aacttgacca aaaagcgggt gacgctgctc 180
attctgctgg tgtgggccat cgccatcttc atggggggccg tccccacnct gggatggaat 240
tgccctctgca acatctcggc ctgctcttct ctgggtccca ttacagtag gagttacctc 300
atcttctgga ctgtgtccaa cctcctggcc ttcttcatca tgggtggcgg atacgtacgc 360
atctacatgt atgttaaaag gaaaaccaac gtcttatctc cacacaccag tggtccatc 420
agccgccgga gggctcccat gaagctaata aagacagtga tgaccgtctt aggcgccttc 480
gtgggtgtgct ggaccccggg tctggtggtt ctgctgctgg acggcctgaa ctgcaagcag 540
tgtaacgtgc aacacgtgaa gngctggttc ctgctgctcg cactgctcaa ctccgtcatg 600
aaccacctca tctactgccg ctctccnnac tttccatgg 639

<210> 4
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer: JC501-F2

<400> 4
tttttactcg agatttgctg gttattgctg tggaaag

37

<210> 5
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer: JC501-R

<400> 5
ttttttctag acggtcatca ctgtcttcat tagcttc

37

<210> 6
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer: H501-20F

<400> 6
atgcggtgc atagcaacct gacaaaaaag

30

<210> 7
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer: H501-246R

<400> 7
atccgcaggt acaccacaac catgatgagg

30

<210> 8
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer: GT10-F

<400> 8
ttttgagcaa gttcagcctg gttaagt

27

<210> 9
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer: GT10-R

<400> 9
tggcttatga gtatttcttc cagggtta

27

<210> 10
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer: GT10-5KX-b

<400> 10
gggtagtcgg tacctctaga gcaagttcag cc

32

<210> 11
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer: GT10-3BXh

<400> 11
ataacagagg atcctcgagt atttcttcca g

31

<210> 12
<211> 1523
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of the genomic DNA flanking 5' end of the
hedg-5 cDNA insert of pC3-hedg-55 clone and the hedg-5 cDNA

a!
cont

<400> 12
caccttccta acctgagcgg cctagcctgg gaaacaaaca attaaaatgt gcgctaaatg 60
ctgtggtagg aggtcagggg ctatgtcctg gaccaaagga catttgact gagacctgac 120
acttcaggtc ttcaactccc ttgatgggag ttagccagaa cgggcttaga aacagcaatt 180
gatggcttag tgactgattt tacaaatgat atttgtttct tctttaaatt tctttctagg 240
atgttcactt cttctccaca atgaatgagt gtcactatga caagcacatg gacttttttt 300
ataataggag caacactgat actgtcgatg actggacagg aacaaagctt gtgattgttt 360
tgtgtgttgg gacgtttttc tgctgttta tttttttttc taattctctg gtcacgcg 420
cagtgatcaa aaacagaaaa tttcatttcc ctttttacta cctgttggtt aatttagctg 480

ctgccgattt cttcgctgga attgcctatg tattcctgat gtttaacaca ggcccagttt	540
caaaaacttt gactgtcaac cgctggtttc tccgtcaggg gcttctggac agtagcttga	600
ctgcttcctt caccaacttg ctggttatcg ccgtggagag gcacatgtca atcatgagga	660
tgcgggtcca tagcaacctg accaaaaaga gggtgacact gctcattttg cttgtctggg	720
ccatcgccat ttttatgggg gcgggtccca cactgggctg gaattgcctc tgcaacatct	780
ctgcctgctc ttccctggcc cccatttaca gcaggagtta ccttgttttc tggacagtgt	840
ccaacctcat ggccttcctc atcatgggtg tgggtgtacct gcggatctac gtgtacgtca	900
agaggaaaac caacgtcttg tctccgcata caagtgggtc catcagccgc cggaggacac	960
ccatgaagct aatgaagacg gtgatgactg tcttaggggc gtttgtggta tgctggaccc	1020
cgggcctggg ggttctgccc ctcgacggcc tgaactgcag gcagtgtggc gtgcagcatg	1080
tgaaaagggtg gttcctgctg ctggcgctgc tcaactccgt cgtgaacccc atcatctact	1140
cctacaagga cgaggacatg tatggcacca tgaagaagat gatctgctgc ttctctcagg	1200
agaaccacaga gaggcgtccc tctcgcatcc cctccacagt cctcagcagg agtgacacag	1260
gcagccagta catagaggat agtattagcc aagggtgcagt ctgcaataaa agcacttcct	1320
aaactctgga tgctcttygg cccaccacag cctcctctgg gaaaagagct gttaagaatg	1380
attacctgtc tctaacaag cccatgtaca gtgttatttg aggtctccat taatcactgc	1440
tagatttctt taaaaaattt tttttcatag tttaaaagca tgggcagtaa agagaggacc	1500
tgctgcattt agagaaagca cag	1523

<210> 13
 <211> 1357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence of a hEDG-5 cDNA inserted into pcDNA3

<400> 13	
gaattcgcgg ccgcgtcgac gttcacttct ccacaatgaa tgagtgtcac tatgacaagc	60
acatggactt tttttataat aggagcaaca ctgatactgt cgatgactgg acaggaacaa	120
agcttgatgat tgttttgtgt gttgggacgt ttttctgcct gtttattttt ttttctaatt	180
ctctggatcat cgcggcagtg atcaaaaaca gaaaatttca ttcccccttt tactacctgt	240
tggctaattt agctgctgcc gatttcttcg ctggaattgc ctatgtattc ctgatgttta	300

acacaggccc agtttcaaaa actttgactg tcaaccgctg gtttctccgt caggggcttc 360
 tggacagtag cttgactgct tccctcacca acttgctggt tatcgccgtg gagaggcaca 420
 tgtcaatcat gaggatgcgg gtccatagca acctgaccaa aaagaggggtg acactgctca 480
 ttttgcttgt ctggggccatc gccattttta tggggggcggg cccacactg ggctggaatt 540
 gcctctgcaa catctctgcc tgctcttccc tggcccccat ttacagcagg agttaccttg 600
 ttttctggac agtgtccaac ctcatggcct tctcatcat ggttggtggtg tacctgcgga 660
 tctacgtgta cgtcaagagg aaaaccaacg tcttgctctcc gcatacaagt ggggccatca 720
 gccgccggag gacacccatg aagctaata gaacgggtgat gactgtctta ggggcgtttg 780
 tggtagctg gaccccgggc ctggtggttc tgccccctga cggcctgaac tgcaggcagt 840
 gtggcgtgca gcatgtgaaa aggtggttcc tgctgctggc gctgctcaac tccgtcgtga 900
 accccatcat ctactcctac aaggacgagg acatgtatgg caccatgaag aagatgatct 960
 gctgcttctc tcaggagaac ccagagaggc gtccctctcg catccccctc acagtcctca 1020
 gcaggagtga cacaggcagc cagtacatag aggatagtat tagccaaggc gcagtctgca 1080
 ataaaagcac ttcctaaact ctggatgcct ctggggccac ccaggcctcc tctgggaaaa 1140
 gagctgttaa gaatgattac ctgtctctaa caaagcccat gtacagtgtt atttgaggtc 1200
 tccattaatc actgctagat ttctttaaaa aatttttttt catagttaa aagcatgggc 1260
 agtaaagaga ggacctgctg catttagaga aagcacaggc cgacgcggcc gcgaattctt 1320
 ttgcttttta ccttgggaaga aatactcgag catgcat 1357

a1
Cont

<210> 14
 <211> 353
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Predicited amino acid sequence of pC3-hedg-55 clone
 <400> 14

Met	Asn	Glu	Cys	His	Tyr	Asp	Lys	His	Met	Asp	Phe	Phe	Tyr	Asn	Arg
1				5					10					15	

Ser	Asn	Thr	Asp	Thr	Val	Asp	Asp	Trp	Thr	Gly	Thr	Lys	Leu	Val	Ile
			20					25					30		

Val	Leu	Cys	Val	Gly	Thr	Phe	Phe	Cys	Leu	Phe	Ile	Phe	Phe	Ser	Asn	
		35					40					45				
Ser	Leu	Val	Ile	Ala	Ala	Val	Ile	Lys	Asn	Arg	Lys	Phe	His	Phe	Pro	
	50					55					60					
Phe	Tyr	Tyr	Leu	Leu	Ala	Asn	Leu	Ala	Ala	Ala	Asp	Phe	Phe	Ala	Gly	
65					70					75					80	
Ile	Ala	Tyr	Val	Phe	Leu	Met	Phe	Asn	Thr	Gly	Pro	Val	Ser	Lys	Thr	
				85					90					95		
Leu	Thr	Val	Asn	Arg	Trp	Phe	Leu	Arg	Gln	Gly	Leu	Leu	Asp	Ser	Ser	
			100					105					110			
Leu	Thr	Ala	Ser	Leu	Thr	Asn	Leu	Leu	Val	Ile	Ala	Val	Glu	Arg	His	
		115					120					125				
Met	Ser	Ile	Met	Arg	Met	Arg	Val	His	Ser	Asn	Leu	Thr	Lys	Lys	Arg	
	130					135					140					
Val	Thr	Leu	Leu	Ile	Leu	Leu	Val	Trp	Ala	Ile	Ala	Ile	Phe	Met	Gly	
145					150					155					160	
Ala	Val	Pro	Thr	Leu	Gly	Trp	Asn	Cys	Leu	Cys	Asn	Ile	Ser	Ala	Cys	
				165					170					175		
Ser	Ser	Leu	Ala	Pro	Ile	Tyr	Ser	Arg	Ser	Tyr	Leu	Val	Phe	Trp	Thr	
			180					185					190			
Val	Ser	Asn	Leu	Met	Ala	Phe	Leu	Ile	Met	Val	Val	Val	Tyr	Leu	Arg	
		195					200					205				
Ile	Tyr	Val	Tyr	Val	Lys	Arg	Lys	Thr	Asn	Val	Leu	Ser	Pro	His	Thr	
	210					215					220					
Ser	Gly	Ser	Ile	Ser	Arg	Arg	Arg	Thr	Pro	Met	Lys	Leu	Met	Lys	Thr	
225					230					235					240	
Val	Met	Thr	Val	Leu	Gly	Ala	Phe	Val	Val	Cys	Trp	Thr	Pro	Gly	Leu	
				245					250					255		

a!
Cont

Val Val Leu Pro Leu Asp Gly Leu Asn Cys Arg Gln Cys Gly Val Gln
 260 265 270

His Val Lys Arg Trp Phe Leu Leu Leu Ala Leu Leu Asn Ser Val Val
 275 280 285

Asn Pro Ile Ile Tyr Ser Tyr Lys Asp Glu Asp Met Tyr Gly Thr Met
 290 295 300

Lys Lys Met Ile Cys Cys Phe Ser Gln Glu Asn Pro Glu Arg Arg Pro
 305 310 315 320

Ser Arg Ile Pro Ser Thr Val Leu Ser Arg Ser Asp Thr Gly Ser Gln
 325 330 335

Tyr Ile Glu Asp Ser Ile Ser Gln Gly Ala Val Cys Asn Lys Ser Thr
 340 345 350

Ser

<210> 15
 <211> 213
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Predicted amino acid sequence of mouse partial EDG-5 cDNA

<220>
 <221> MISC_FEATURE
 <222> (188)..(210)
 <223> Xaa = unknown

<400> 15

Asn Thr Gly Pro Val Ser Lys Thr Leu Thr Val Asn Arg Trp Phe Leu
 1 5 10 15

Arg Gln Gly Leu Leu Asp Thr Ser Leu Thr Ala Ser Leu Ala Asn Leu
 20 25 30

Leu Val Ile Ala Val Glu Arg His Met Ser Ile Met Arg Met Arg Val

35

40

45

His Ser Asn Leu Thr Lys Lys Arg Val Thr Leu Leu Ile Leu Leu Val
50 55 60

Trp Ala Ile Ala Ile Phe Met Gly Ala Val Pro Thr Leu Gly Trp Asn
65 70 75 80

Cys Leu Cys Asn Ile Ser Ala Cys Ser Ser Leu Ala Pro Ile Tyr Ser
85 90 95

Arg Ser Tyr Leu Ile Phe Trp Thr Val Ser Asn Leu Leu Ala Phe Phe
100 105 110

Ile Met Val Ala Val Tyr Val Arg Ile Tyr Met Tyr Val Lys Arg Lys
115 120 125

Thr Asn Val Leu Ser Pro His Thr Ser Gly Ser Ile Ser Arg Arg Arg
130 135 140

Ala Pro Met Lys Leu Met Lys Thr Val Met Thr Val Leu Gly Ala Phe
145 150 155 160

Val Val Cys Trp Thr Pro Gly Leu Val Val Leu Leu Leu Asp Gly Leu
165 170 175

Asn Cys Lys Gln Cys Asn Val Gln His Val Lys Xaa Trp Phe Leu Leu
180 185 190

Leu Ala Leu Leu Asn Ser Val Met Asn Pro Leu Ile Tyr Cys Arg Ser
195 200 205

Pro Xaa Phe Pro Trp
210

<210> 16

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer: HE5-216F

<400> 16
 atgaatgagt gtcactatga caag 24

<210> 17
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer: HE5-1011R

<400> 17
 ataccacaaa cgcccctaag acagtcacatca ccgtcttc 38

<210> 18
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer: HE5-982F

<400> 18
 tgatgactgt cttaggggcg tttgtggtat gctggacc 38

<210> 19
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer: HE5-1322R

<400> 19
 ttaggaagtg cttttattgc agactgc 27

<210> 20
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer: HE5-KZKF

<400> 20
 tttaaactcg agccaccatg aatgagtgtc actatgac 38

<210> 21
 <211> 39
 <212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer: HE5-Kpn1322R

<400> 21

tatataggta ccttaggaag tgcttttatt gcagactgc

39

<210> 22

<211> 2033

<212> DNA

<213> Artificial Sequence

<220>

<223> Full length mEDG-5 cDNA

<400> 22

gcacagttct tgtccacat gaatgagtgt cactatgaca agcgcatgga ctttttctac 60
aacaggagca acacagacac agcggacgag tggacaggga caaagcttgt gatcgctctg 120
tgcggtggga cgttcttctg cctctttata ttttttctta actccctggc cattgctgcg 180
gtgatcacia accggaagt ccactttccc ttctactacc tgctggctaa cttagctgct 240
gcggatttct tcgccggaat cgcttacgtg ttctgatgtg ttaacactgg cccgggtgctg 300
aaaacgttga ccgtcaaccg ctggttcctc cgccaggggc tcctagacac cagcctgact 360
gcctccctgg ccaatttgct ggttattgct gtggaaagac acatgtcaat catgaggatg 420
agagtccaca gcaacttgac caaaaagcgg gtgacgctgc tcattctgct ggtgtggggc 480
atcgccatct tcatgggggc cgtccccacg ctgggatgga attgcctctg caacatctcg 540
gcctgctctt ctctggctcc catttacagt aggagttacc tcattttctg gactgtgtcc 600
aacctcctgg ccttcttcat catggtggcg gtatacgtac gcatctacat gtatgttaaa 660
aggaaaacca acgtcttata tccacacacc agtggctcca tcagccgccg gagggctccc 720
atgaagctaa tgaagacagt gatgaccgtc ttaggcgcct tcgtggtgtg ctggaccccc 780
gggtctggtg ttctgctgct ggacggcctg aactgcaagc agtgtaacgt gcaacacgtg 840
aagcgctggc tcctgctgct cgcactgctc aactccgtca tgaaccccat catctactcg 900
tacaaggacg aggacatgta caacaccatg cggaagatga tctgctgtgc cctgcaggac 960
agcaataccg agaggcgccc ctcccgaac ccctccacca tccacagcag gagcgagacg 1020
ggcagccagt acctggagga cagcatcagc cagggcccgg tgtgcaataa aaacggctcc 1080
taagccacgg acgcctccgc cctcttcccc tggggaaaga gctgttaagc gtcctcacct 1140

a!
Cont.

gtctcacaaa gcacgtggac agggttgttt gagggctcca tgcattcactt ctgggggcttt 1200
 taagttttca tgggtcaagga aaatagattt acggcggttta gtaaagcgca caggaaaggg 1260
 agagatgagc agtgggttcc ggcttgtctg tgatccgctc ccaacatcct ccagctcttg 1320
 cgagagcatg ctgggctctg tcaccatctt gccaccattg tctgtgtgtt ttcaatgatg 1380
 gtgttgaaag tcctaggtca aaagaaagta gtaaataatg gtacctgagc cccccattgt 1440
 gtggctacta gattctgtag ttgtttccgc atgggtttta aatgttcaga aaaatatttt 1500
 agcagtgaac tttgatttcc tcagagaagc catggccagg agctaggtgg gcaactgtat 1560
 agtagagtaa gtgatgatat tgaccggtag gttgaacttc ttccaaatag cgtcaaatat 1620
 gagcacgatt agatcttcag tcttggttat caggataccg ctgaggggct tgctggatcc 1680
 caagtgcaaa gtaattgcac atcgagtatt ttaaccaaag ctgccagcgt attctatctt 1740
 gtggactgca ttttgatctt gtatttttct ctttcaaaga cctctgaaag gtagatcagt 1800
 taaaaacaaa aatagtgttc atacacatag gctactgacc agtgttttcg gtgtaagacg 1860
 tttagagtgt atctgacaaa gtaagaataa cttcaaggca ggcactatgg tatttatgta 1920
 gcttgcaaac gtttacatgt tctctctctc tctctctctc ccctctgctg ttgtgatgta 1980
 acatttatgt gcacaaacta cttgtaataa aatattttta gaagcaaaaa aaa 2033

<210> 23
 <211> 354
 <212> PRT
 <213> Mouse

<400> 23

Met Asn Glu Cys His Tyr Asp Lys Arg Met Asp Phe Phe Tyr Asn Arg
 1 5 10 15

Ser Asn Thr Asp Thr Ala Asp Glu Trp Thr Gly Thr Lys Leu Val Ile
 20 25 30

Val Leu Cys Val Gly Thr Phe Phe Cys Leu Phe Ile Phe Phe Ser Asn
 35 40 45

Ser Leu Val Ile Ala Ala Val Ile Thr Asn Arg Lys Phe His Phe Pro
 50 55 60

Phe Tyr Tyr Leu Leu Ala Asn Leu Ala Ala Ala Asp Phe Phe Ala Gly
65 70 75 80

Ile Ala Tyr Val Phe Leu Met Phe Asn Thr Gly Pro Val Ser Lys Thr
85 90 95

Leu Thr Val Asn Arg Trp Phe Leu Arg Gln Gly Leu Leu Asp Thr Ser
100 105 110

Leu Thr Ala Ser Leu Ala Asn Leu Leu Val Ile Ala Val Glu Arg His
115 120 125

Met Ser Ile Met Arg Met Arg Val His Ser Asn Leu Thr Lys Lys Arg
130 135 140

Val Thr Leu Leu Ile Leu Leu Val Trp Ala Ile Ala Ile Phe Met Gly
145 150 155 160

Ala Val Pro Thr Leu Gly Trp Asn Cys Leu Cys Asn Ile Ser Ala Cys
165 170 175

Ser Ser Leu Ala Pro Ile Tyr Ser Arg Ser Tyr Leu Ile Phe Trp Thr
180 185 190

Val Ser Asn Leu Leu Ala Phe Phe Ile Met Val Ala Val Tyr Val Arg
195 200 205

Ile Tyr Met Tyr Val Lys Arg Lys Thr Asn Val Leu Ser Pro His Thr
210 215 220

Ser Gly Ser Ile Ser Arg Arg Arg Ala Pro Met Lys Leu Met Lys Thr
225 230 235 240

Val Met Thr Val Leu Gly Ala Phe Val Val Cys Trp Thr Pro Gly Leu
245 250 255

Val Val Leu Leu Leu Asp Gly Leu Asn Cys Lys Gln Cys Asn Val Gln
260 265 270

His Val Lys Arg Trp Phe Leu Leu Leu Ala Leu Leu Asn Ser Val Met
275 280 285

Asn Pro Ile Ile Tyr Ser Tyr Lys Asp Glu Asp Met Tyr Asn Thr Met
 290 295 300

Arg Lys Met Ile Cys Cys Ala Leu Gln Asp Ser Asn Thr Glu Arg Arg
 305 310 315 320

Pro Ser Arg Asn Pro Ser Thr Ile His Ser Arg Ser Glu Thr Gly Ser
 325 330 335

Gln Tyr Leu Glu Asp Ser Ile Ser Gln Gly Pro Val Cys Asn Lys Asn
 340 345 350

Gly Ser

<210> 24
 <211> 1062
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> cDNA sequence of clone pC3-hEDG5#3.4 from the region encoding a hEDG5 polypeptide

<400> 24
 atgaatgagt gtcactatga caagcacatg gacttttttt ataataggag caacactgat 60
 actgtcgatg actggactgg aacaaagctt gtgattgttt tgtgtgttgg gacgtttttc 120
 tgcctgttta tttttttttc taattctctg gtcacgcg cagtgatcaa aaacagaaaa 180
 tttcatttcc ctttctacta cctgttggct aatttggctg ctgccgattt cttcgctgga 240
 attgcctatg tattcctgat gtttaacaca ggcccagttt caaaaacttt gactgtcaac 300
 cgctggtttc tccgtcaggg gcttctggac agtagcttga ctgcttcctt caccaacttg 360
 ctggttatcg ccgtggagag gcacatgtca atcatgagga tgcgggtcca tagcaacctg 420
 accaaaaaga gggtgacact gctcattttg cttgtctggg ccacgcgcat ttttatgggg 480
 gcgggtccca cactgggctg gaattgcctc tgcaacatct ctgcctgctc ttccctggcc 540
 cccatttaca gcaggagtta cttgtttttc tggacagtgt ccaacctcat ggccttcctc 600
 atcatgggtt tggtgtacct gcggatctac gtgtacgtca agaggaaaac caacgtcttg 660
 tctccgcata caagtgggtc catcagccgc cggaggacac ccatgaagct aatgaagacg 720

gtaatgactg tcttaggggc gtttgtggta tgctggaccc cgggcctggt ggttctgctc	780
ctcgacggcc tgaactgcag gcagtgtggc gtgcagcatg tgaaaagggtg gttcctgctg	840
ctggcgctgc tcaactccgt cgtgaaccct atcatctact cctacaagga cgaggacatg	900
tatggcacca tgaagaagat gatctgctgc ttctctcagg agaaccaga gaggcgtccc	960
tctcgcatcc cctccacagt cctcagcagg agtgacacag gcagccagta catagaggat	1020
agtattagcc aagggtgcagt ctgcaataaa agcacttcct aa	1062

<210> 25
 <211> 1062
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> cDNA sequence of clone pC3-hEDG5#28 from the region encoding a hEDG5 polypeptide

<400> 25	
atgaatgagt gtcactatga caagcacatg gacttttttt ataatagggg caacactgat	60
actgtcgatg actggacagg aacaaagctt gtgattgttt tgtgtgttgg gacgtttttc	120
tgccgtgttta tttttttttc taattctctg gtcacgcggc cagtgatcaa aaacagaaaa	180
tttcatttcc ctttctacta cctgttggct aatttagctg ctgccgattt cttecgctgga	240
attgcctatg tattcctgat gtttaacaca ggcccagttt caaaaacttt gactgtcaac	300
cgctgggttc tccgtcaggg gcttctggac agtagcttga ctgcttcctt caccaacttg	360
ctggttatcg ccgtggagag gcacatgtca atcatgagga tgcgggtcca tagcaacctg	420
accaaaaaga gggtgacact gctcattttg cttgtctggg ccatcgccat ttttatgggg	480
gcgggtcccca cactgggctg gaattgcctc tgcaacatct ctgcctgctc ttccctggcc	540
cccatttaca gcaggagtta cttgtttttc tggacagtgt ccaacctcat ggccttcctc	600
atcatggttg tgggtgtacct gcggatctac gtgtacgtca agaggaaaac caacgtcttg	660
tetccgcata caagtgggtc catcagccgc cggaggacac ccatgaagct aatgaagacg	720
gtgatgactg tcttaggggc gtttgtggta tgctggaccc cgggcctggt ggttctgctc	780
ctcgacggcc tgaactgcag gcagtgtggc gtgcagcatg tgaaaagggtg gttcctgctg	840
ctggcgctgc tcaactccgt cgtgaacccc atcatctact cctacaagga cgaggacatg	900
tatggcacca tgaagaagat gatctgctgc ttctctcagg agaaccaga gaggcgtccc	960

a!
 Cont

tctcgcatcc cctccacagt cctcagcagg agtgacacag gcagccagta catagaggat 1020
 agtatttagcc aagggtgcagt ctgcaataaa agcacttcct aa 1062

<210> 26
 <211> 1523
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Complementary strand nucleotide sequence of the genomic DNA
 flanking 5' end of the hedg-5 cDNA insert of pC3-hedg-55 clone
 and the hedg-5 cDNA

<400> 26
 gtggaaggat tggactcgcc ggatcggacc ctttgtttgt taattttaca cgcgatttac 60
 gacaccatcc tccagtcccc gatacaggac ctggtttcct gtaaacgtga ctctggactg 120
 tgaagtccag aagttgaggg aactaccctc aatcgggtctt gcccgaaatct ttgtcgttaa 180
 ctaccgaatc actgactaaa atgtttacta taaacaaaga agaaatttaa agaaagatcc 240
 tacaagtgaa gaagaggtgt tacttactca cagtgatact gttcgtgtac ctgaaaaaaaa 300
 tattatcctc gttgtgacta tgacagctac tgacctgtcc ttgtttcgaa cactaacaaa 360
 acacacaacc ctgcaaaaaag acggacaaat aaaaaaaaaag attaagagac cagtagcgcc 420
 gtcactagtt tttgtctttt aaagtaaagg ggaaaatgat ggacaaccga ttaaatacgac 480
 gacgggctaaa gaagcgacct taacggatac ataaggacta caaattgtgt ccgggtcaaa 540
 gtttttgaaa ctgacagttg gcgaccaaag aggcagtccc cgaagacctg tcatcgaact 600
 gacgaaggga gtggttgaac gaccaatagc ggcacctctc cgtgtacagt tagtactcct 660
 acgcccaggt atcgttggac tggtttttct ccactgtga cgagtaaaac gaacagaccc 720
 ggtagcggtg aaaatacccc cgccaggggt gtgacccgac cttaacggag acgttgtaga 780
 gacggacgag aagggaccgg gggtaaatgt cgtcctcaat ggaacaaaag acctgtcaca 840
 gggttgagta ccggaaggag tagtaccaac accacatgga cgcctagatg cacatgcagt 900
 tctccttttg gttgcagaac agaggcgtat gttcaccag gtagtcggcg gcctcctgtg 960
 ggtacttcga ttacttctgc cactactgac agaatccccg caaacaccat acgacctggg 1020
 gcccggaacca ccaagacggg gagctgccgg acttgacgtc cgtcacaccg cacgtcgtac 1080
 acttttccac caaggacgac gaccgcgacg agttgaggca gcacttgggg tagtagatga 1140
 ggatgttcct gtcctgttac ataccgtggt acttcttcta ctagacgacg aagagagtcc 1200

a!
 cont

tcttggtct ctccgcagg agagcgtagg ggaggtgtca ggagtcgtcc tcactgtgtc 1260
 cgtcggtcat gtatctccta tcataatcgg ttccacgtca gacgttatatt tcgtgaagga 1320
 tttgagacct acggagarcc gggtaggtcc ggaggagacc cttttctcga caattcttac 1380
 taatggacag agattgtttc gggtagcatgt cacaataaac tccagaggta attagtgtacg 1440
 atctaaagaa attttttaaa aaaaagtatc aaattttcgt acccgtcatt tctctcctgg 1500
 acgacgtaaa tctctttcgt gtc 1523

<210> 27
 <211> 353
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Predicted amino acid sequence of hEDG5 encoded by clone
 pC3-hEDG5#3.4

<400> 27

Met Asn Glu Cys His Tyr Asp Lys His Met Asp Phe Phe Tyr Asn Arg
 1 5 10 15

Ser Asn Thr Asp Thr Val Asp Asp Trp Thr Gly Thr Lys Leu Val Ile
 20 25 30

Val Leu Cys Val Gly Thr Phe Phe Cys Leu Phe Ile Phe Phe Ser Asn
 35 40 45

Ser Leu Val Ile Ala Ala Val Ile Lys Asn Arg Lys Phe His Phe Pro
 50 55 60

Phe Tyr Tyr Leu Leu Ala Asn Leu Ala Ala Ala Asp Phe Phe Ala Gly
 65 70 75 80

Ile Ala Tyr Val Phe Leu Met Phe Asn Thr Gly Pro Val Ser Lys Thr
 85 90 95

Leu Thr Val Asn Arg Trp Phe Leu Arg Gln Gly Leu Leu Asp Ser Ser
 100 105 110

Leu Thr Ala Ser Leu Thr Asn Leu Leu Val Ile Ala Val Glu Arg His
 115 120 125

Met Ser Ile Met Arg Met Arg Val His Ser Asn Leu Thr Lys Lys Arg
130 135 140

Val Thr Leu Leu Ile Leu Leu Val Trp Ala Ile Ala Ile Phe Met Gly
145 150 155 160

Ala Val Pro Thr Leu Gly Trp Asn Cys Leu Cys Asn Ile Ser Ala Cys
165 170 175

Ser Ser Leu Ala Pro Ile Tyr Ser Arg Ser Tyr Leu Val Phe Trp Thr
180 185 190

Val Ser Asn Leu Met Ala Phe Leu Ile Met Val Val Val Tyr Leu Arg
195 200 205

Ile Tyr Val Tyr Val Lys Arg Lys Thr Asn Val Leu Ser Pro His Thr
210 215 220

Ser Gly Ser Ile Ser Arg Arg Arg Thr Pro Met Lys Leu Met Lys Thr
225 230 235 240

Val Met Thr Val Leu Gly Ala Phe Val Val Cys Trp Thr Pro Gly Leu
245 250 255

Val Val Leu Leu Leu Asp Gly Leu Asn Cys Arg Gln Cys Gly Val Gln
260 265 270

His Val Lys Arg Trp Phe Leu Leu Leu Ala Leu Leu Asn Ser Val Val
275 280 285

Asn Pro Ile Ile Tyr Ser Tyr Lys Asp Glu Asp Met Tyr Gly Thr Met
290 295 300

Lys Lys Met Ile Cys Cys Phe Ser Gln Glu Asn Pro Glu Arg Arg Pro
305 310 315 320

Ser Arg Ile Pro Ser Thr Val Leu Ser Arg Ser Asp Thr Gly Ser Gln
325 330 335

Tyr Ile Glu Asp Ser Ile Ser Gln Gly Ala Val Cys Asn Lys Ser Thr

340

345

350

Ser

<210> 28
 <211> 353
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Predicted amino acid sequence of hEDG5 encoded by clone
 pC3-hEDG5#28

<400> 28

Met Asn Glu Cys His Tyr Asp Lys His Met Asp Phe Phe Tyr Asn Arg
 1 5 10 15

Gly Asn Thr Asp Thr Val Asp Asp Trp Thr Gly Thr Lys Leu Val Ile
 20 25 30

Val Leu Cys Val Gly Thr Phe Phe Cys Leu Phe Ile Phe Phe Ser Asn
 35 40 45

Ser Leu Val Ile Ala Ala Val Ile Lys Asn Arg Lys Phe His Phe Pro
 50 55 60

Phe Tyr Tyr Leu Leu Ala Asn Leu Ala Ala Ala Asp Phe Phe Ala Gly
 65 70 75 80

Ile Ala Tyr Val Phe Leu Met Phe Asn Thr Gly Pro Val Ser Lys Thr
 85 90 95

Leu Thr Val Asn Arg Trp Phe Leu Arg Gln Gly Leu Leu Asp Ser Ser
 100 105 110

Leu Thr Ala Ser Leu Thr Asn Leu Leu Val Ile Ala Val Glu Arg His
 115 120 125

Met Ser Ile Met Arg Met Arg Val His Ser Asn Leu Thr Lys Lys Arg
 130 135 140

Val Thr Leu Leu Ile Leu Leu Val Trp Ala Ile Ala Ile Phe Met Gly

145		150		155		160
Ala Val Pro Thr	Leu Gly Trp Asn Cys	Leu Cys Asn Ile Ser	Ala Cys			
	165	170	175			
Ser Ser Leu Ala Pro Ile Tyr Ser Arg Ser Tyr Leu Val Phe Trp Thr	180	185	190			
Val Ser Asn Leu Met Ala Phe Leu Ile Met Val Val Val Tyr Leu Arg	195	200	205			
Ile Tyr Val Tyr Val Lys Arg Lys Thr Asn Val Leu Ser Pro His Thr	210	215	220			
Ser Gly Ser Ile Ser Arg Arg Arg Thr Pro Met Lys Leu Met Lys Thr	225	230	235	240		
Val Met Thr Val Leu Gly Ala Phe Val Val Cys Trp Thr Pro Gly Leu	245	250	255			
Val Val Leu Leu Leu Asp Gly Leu Asn Cys Arg Gln Cys Gly Val Gln	260	265	270			
His Val Lys Arg Trp Phe Leu Leu Leu Ala Leu Leu Asn Ser Val Val	275	280	285			
Asn Pro Ile Ile Tyr Ser Tyr Lys Asp Glu Asp Met Tyr Gly Thr Met	290	295	300			
Lys Lys Met Ile Cys Cys Phe Ser Gln Glu Asn Pro Glu Arg Arg Pro	305	310	315	320		
Ser Arg Ile Pro Ser Thr Val Leu Ser Arg Ser Asp Thr Gly Ser Gln	325	330	335			
Tyr Ile Glu Asp Ser Ile Ser Gln Gly Ala Val Cys Asn Lys Ser Thr	340	345	350			
Ser						

a!
Cont

<210> 29
<211> 353
<212> PRT
<213> Artificial Sequence

<220>
<223> Predicted amino acid sequence of hEDG5 encoded by clone
pC3-hEdg5-3

<400> 29

Met Asn Glu Cys His Tyr Asp Lys His Met Asp Phe Phe Tyr Asn Arg
1 5 10 15

Ser Asn Thr Asp Thr Val Asp Asp Trp Thr Gly Thr Lys Leu Val Ile
20 25 30

Val Leu Cys Val Gly Thr Phe Phe Cys Leu Phe Ile Phe Phe Ser Asn
35 40 45

Ser Leu Val Ile Ala Ala Val Ile Lys Asn Arg Lys Phe His Phe Pro
50 55 60

Phe Tyr Tyr Leu Leu Ala Asn Leu Ala Ala Ala Asp Phe Phe Ala Gly
65 70 75 80

Ile Ala Tyr Val Phe Leu Met Phe Asn Thr Gly Pro Val Ser Lys Thr
85 90 95

Leu Thr Val Asn Arg Trp Phe Leu Arg Gln Gly Leu Leu Asp Ser Ser
100 105 110

Leu Thr Ala Ser Leu Thr Asn Leu Leu Val Ile Ala Val Glu Arg His
115 120 125

Met Ser Ile Met Arg Met Arg Val His Ser Asn Leu Thr Lys Lys Arg
130 135 140

Val Thr Leu Leu Ile Leu Leu Val Trp Ala Ile Ala Ile Phe Met Gly
145 150 155 160

Ala Val Pro Thr Leu Gly Trp Asn Cys Leu Cys Asn Ile Ser Ala Cys
165 170 175

Ser Ser Leu Ala Pro Ile Tyr Ser Arg Ser Tyr Leu Val Phe Trp Thr
180 185 190

Val Ser Asn Leu Met Ala Phe Leu Ile Met Val Val Val Tyr Leu Arg
195 200 205

Ile Tyr Val Tyr Val Lys Arg Lys Thr Asn Val Leu Ser Pro His Thr
210 215 220

Ser Gly Ser Ile Ser Arg Arg Arg Thr Pro Met Lys Leu Met Lys Thr
225 230 235 240

Val Met Thr Val Leu Gly Ala Phe Val Val Cys Trp Thr Pro Gly Leu
245 250 255

Val Val Leu Pro Leu Asp Gly Leu Asn Cys Arg Gln Cys Gly Val Gln
260 265 270

His Val Lys Arg Trp Phe Leu Leu Leu Ala Leu Leu Asn Ser Val Val
275 280 285

Asn Pro Ile Ile Tyr Ser Tyr Lys Asp Glu Asp Met Tyr Gly Thr Met
290 295 300

Lys Lys Met Ile Cys Cys Phe Ser Gln Glu Asn Pro Glu Arg Arg Pro
305 310 315 320

Ser Arg Ile Pro Ser Thr Val Leu Ser Arg Ser Asp Thr Gly Ser Gln
325 330 335

Tyr Ile Glu Asp Ser Ile Ser Gln Gly Ala Val Cys Asn Lys Ser Thr
340 345 350

Ser